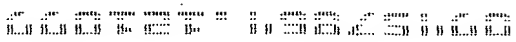
uence Range: 1 to 5578



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         10        20        30        40        50        60        70        80        90       100       110       120
         *         *         *         *         *         *         *         *         *         *         *         *
GACCAATCGGAGTGTGGTGAATTTTTGGAAAATATTTTGTGCGGTTCCTTTAGTTGTGTAATATAGTACTTTAGTTACAAATTTGGAATAATTTGGCAGCAAAACCATCTGCAGCAACAA

        130       140       150       160       170       180       190       200       210       220
         *         *         *         *         *         *         *         *         *         *
AATCATCTGCAGCTGCGAAATCATCTGCAGCAGCAAAAGCATCTTCAGGAGCGAGAAAAGCCCCAAATAATGTGAG ATG GCA GTT GAC GTC CGA ATC GCT GCC TTC CTG
                                                                                Met Ala Val Asp Val Arg Ile Ala Ala Phe Leu>

230       240       250       260       270       280       290       300       310
 *         *         *         *         *         *         *         *         *
CTG GTG TTT ATA GCG CCT GCA GTT TTA GCT CAA GAG AGA TGT GGG TAT ATG ACC GCC ATC CCA AGG CTA CCA CGA CCG GAT AAT TTG CCA
Leu Val Phe Ile Ala Pro Ala Val Leu Ala Gln Glu Arg Cys Gly Tyr Met Thr Ala Ile Pro Arg Leu Pro Arg Pro Asp Asn Leu Pro>

320       330       340       350       360       370       380       390       400
 *         *         *         *         *         *         *         *         *
GTA CTA AAT TTT GAA GGC CAG ACA TGG AGT CAG AGG CCC CTG CTC CCC GCC CCG GAG CGG GAT GAC CTG TGC ATG GAC GCC TAC CAC GTG
Val Leu Asn Phe Glu Gly Gln Thr Trp Ser Gln Arg Pro Leu Leu Pro Ala Pro Glu Arg Asp Asp Leu Cys Met Asp Ala Tyr His Val>

410       420       430       440       450       460       470       480       490
 *         *         *         *         *         *         *         *         *
ATA ACA GCC AAC CTC GGC ACG CAG GTC ATC TAC ATG GAT GAA GAG ATA GAA GAC GAA ATC ACC ATC GCC ATA CTT AAT TAT AAC GGA CCA
Ile Thr Ala Asn Leu Gly Thr Gln Val Ile Tyr Met Asp Glu Glu Ile Glu Asp Glu Ile Thr Ile Ala Ile Leu Asn Tyr Asn Gly Pro>

500       510       520       530       540       550       560       570       580
 *         *         *         *         *         *         *         *         *
TCA ACT CCG TTC ATT GAA CTG CCA TTT TTA TCC GGT TCG TAC AAT CTG CTG ATG CCG GTC ATC AGG AGA GTT GAC AAC GGG AGT GCA TCT
Ser Thr Pro Phe Ile Glu Leu Pro Phe Leu Ser Gly Ser Tyr Asn Leu Leu Met Pro Val Ile Arg Arg Val Asp Asn Gly Ser Ala Ser>

590       600       610       620       630       640       650       660       670
 *         *         *         *         *         *         *         *         *
CAT CAT CAC GCA AGA CAG CAT TAC GAG TTG CCC GGC ATG CAG CAG TAC ATG TTC AAT GTG CGC GTG GAC GGC CAG TCG CTG GTG GCA GGC
His His His Ala Arg Gln His Tyr Glu Leu Pro Gly Met Gln Gln Tyr Met Phe Asn Val Arg Val Asp Gly Gln Ser Leu Val Ala Gly>

680       690       700       710       720       730       740       750       760
 *         *         *         *         *         *         *         *         *
GTG TCT CTC GCT ATC GTC AAC ATA GAT GAC AAC GCG CCC ATC ATA CAA AAC TTC GAG CCT TGC CGG GTT CCT GAA CTG GGC GAG CCA GGG
Val Ser Leu Ala Ile Val Asn Ile Asp Asp Asn Ala Pro Ile Ile Gln Asn Phe Glu Pro Cys Arg Val Pro Glu Leu Gly Glu Pro Gly>

770       780       790       800       810       820       830       840       850
 *         *         *         *         *         *         *         *         *
TTG ACA GAA TGC ACA TAC CAA GTA TCG GAC GCG GAC GGA CGG ATC AGC ACA GAG TTC ATG ACG TTC AGG ATC GAC AGC GTT CGT GGC GAC
Leu Thr Glu Cys Thr Tyr Gln Val Ser Asp Ala Asp Gly Arg Ile Ser Thr Glu Phe Met Thr Phe Arg Ile Asp Ser Val Arg Gly Asp>

860       870       880       890       900       910       920       930       940
 *         *         *         *         *         *         *         *         *
GAG GAG ACC TTC TAC ATC GAA CGG ACG AAT ATC CCC AAC CAA TGG ATG TGG CTA AAT ATG ACC ATA GGC GTT AAT ACC TCG CTC AAC TTC
Glu Glu Thr Phe Tyr Ile Glu Arg Thr Asn Ile Pro Asn Gln Trp Met Trp Leu Asn Met Thr Ile Gly Val Asn Thr Ser Leu Asn Phe>

950       960       970       980       990      1000      1010      1020      1030
 *         *         *         *         *         *         *         *         *
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Fig 1.

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   GTC ACC AGT CCG CTG CAT ATA TTC AGC GTG ACA GCC CTG GAC TCG CTC CCG AAC ACC CAC ACG GTG ACT ATG ATG GTG CAA GTG GCG AAT
   Val Thr Ser Pro Leu His Ile Phe Ser Val Thr Ala Leu Asp Ser Leu Pro Asn Thr His Thr Val Thr Met Met Val Gln Val Ala Asn>

1040        1050        1060        1070        1080        1090        1100        1110        1120
   *           *           *           *           *           *           *           *           *
   GTG AAC AGC CGT CCG CCG CGC TGG CTG GAG ATC TTC GCT GTC CAA CAG TTT GAA GAG AAA TCT TAC CAA AAC TTC ACA GTG AGG GCG ATC
   Val Asn Ser Arg Pro Pro Arg Trp Leu Glu Ile Phe Ala Val Gln Gln Phe Glu Glu Lys Ser Tyr Gln Asn Phe Thr Val Arg Ala Ile>

1130        1140        1150        1160        1170        1180        1190        1200        1210
   *           *           *           *           *           *           *           *           *
   GAC GGA GAC ACT GAG ATC AAT ATG CCT ATC AAC TAC AGG CTG ATC ACA AAT GAG GAA GAC ACA TTC TTC AGC ATT GAG GCC CTG CCT GGT
   Asp Gly Asp Thr Glu Ile Asn Met Pro Ile Asn Tyr Arg Leu Ile Thr Asn Glu Glu Asp Thr Phe Phe Ser Ile Glu Ala Leu Pro Gly>

1220        1230        1240        1250        1260        1270        1280        1290        1300
   *           *           *           *           *           *           *           *           *
   GGA AAA AGC GGG GCT GTA TTC CTC GTG TCG CCA ATT GAC CGC GAC ACA CTG CAA CGA GAG GTG TTT CCA CTT ACG ATC GTC GCT TAC AAA
   Gly Lys Ser Gly Ala Val Phe Leu Val Ser Pro Ile Asp Arg Asp Thr Leu Gln Arg Glu Val Phe Pro Leu Thr Ile Val Ala Tyr Lys>

1310        1320        1330        1340        1350        1360        1370        1380        1390
   *           *           *           *           *           *           *           *           *
   TAT GAT GAG GAG GCC TTC TCC ACA TCA ACA AAC GTG GTC ATC ATT GTG ACA GAC ATC AAC GAC CAA AGA CCT GAA CCT ATA CAC AAG GAA
   Tyr Asp Glu Glu Ala Phe Ser Thr Ser Thr Asn Val Val Ile Ile Val Thr Asp Ile Asn Asp Gln Arg Pro Glu Pro Ile His Lys Glu>

1400        1410        1420        1430        1440        1450        1460        1470        1480
   *           *           *           *           *           *           *           *           *
   TAT CGA CTG GCA ATC ATG GAG GAG ACG CCC CTG ACC CTC AAC TTC GAT AAA GAA TTC GGA TTT CAT GAT AAG GAT TTA GGT CAA AAC GCT
   Tyr Arg Leu Ala Ile Met Glu Glu Thr Pro Leu Thr Leu Asn Phe Asp Lys Glu Phe Gly Phe His Asp Lys Asp Leu Gly Gln Asn Ala>

1490        1500        1510        1520        1530        1540        1550        1560        1570
   *           *           *           *           *           *           *           *           *
   CAG TAC ACG GTG CGT CTA GAG AGC GTG GAC CCT CCA GGC GCT GCT GAG GCA TTC TAC ATA GCG CCT GAA GTC GGC TAC CAG CGA CAG ACC
   Gln Tyr Thr Val Arg Leu Glu Ser Val Asp Pro Pro Gly Ala Ala Glu Ala Phe Tyr Ile Ala Pro Glu Val Gly Tyr Gln Arg Gln Thr>

1580        1590        1600        1610        1620        1630        1640        1650        1660
   *           *           *           *           *           *           *           *           *
   TTC ATC ATG GGC ACC CTC AAT CAC TCC ATG CTG GAT TAC GAA GTG CCA GAG TTT CAG AGT ATT ACG ATT CGG GTG GTA GCG ACC GAC AAC
   Phe Ile Met Gly Thr Leu Asn His Ser Met Leu Asp Tyr Glu Val Pro Glu Phe Gln Ser Ile Thr Ile Arg Val Val Ala Thr Asp Asn>

1670        1680        1690        1700        1710        1720        1730        1740        1750
   *           *           *           *           *           *           *           *           *
   AAC GAC ACG AGG CAC GTG GGC GTC GCG TTG GTT CAC ATT GAC CTC ATC AAT TGG AAC GAT GAG CAG CCG ATC TTC GAA CAC GCC GTG CAG
   Asn Asp Thr Arg His Val Gly Val Ala Leu Val His Ile Asp Leu Ile Asn Trp Asn Asp Glu Gln Pro Ile Phe Glu His Ala Val Gln>

1760        1770        1780        1790        1800        1810        1820        1830        1840
   *           *           *           *           *           *           *           *           *
   ACC GTC ACC TTC GAC GAG ACT GAA GGC GAG GGG TTC TTC GTC GCC AAG GCG GTT GCA CAC GAC AGA GAC ATC GGG GAT GTC GTC GAG CAT
   Thr Val Thr Phe Asp Glu Thr Glu Gly Glu Gly Phe Phe Val Ala Lys Ala Val Ala His Asp Arg Asp Ile Gly Asp Val Val Glu His>

1850        1860        1870        1880        1890        1900        1910        1920        1930
   *           *           *           *           *           *           *           *           *
   ACT TTA TTG GGT AAC GCT GTT AAC TTC CTG ACC ATC GAC AAA CTC ACC GGC GAC ATC CGC GTC TCA GCT AAC GAC TCC TTC AAC TAC CAT
   Thr Leu Leu Gly Asn Ala Val Asn Phe Leu Thr Ile Asp Lys Leu Thr Gly Asp Ile Arg Val Ser Ala Asn Asp Ser Phe Asn Tyr His>

1940        1950        1960        1970        1980        1990        2000        2010        2020
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Fig. 1 (Con't)

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CGA GAA AGT GAA TTA TTT GTG CAG GTG CGA GCT ACA GAC ACG CTG GGC GAA CCC TTC CAC ACG GCG ACG TCA CAG CTG GTC ATA CGA CTA
Arg Glu Ser Glu Leu Phe Val Gln Val Arg Ala Thr Asp Thr Leu Gly Glu Pro Phe His Thr Ala Thr Ser Gln Leu Val Ile Arg Leu>

2030        2040        2050        2060        2070        2080        2090        2100        2110
AAT GAC ATC AAC AAC ACG CCA CCC ACC TTA CGG CTG CCT CGA GGC AGT CCC CAA GTG GAG GAG AAC GTG CCT GAT GGC CAC GTC ATC ACC
Asn Asp Ile Asn Asn Thr Pro Pro Thr Leu Arg Leu Pro Arg Gly Ser Pro Gln Val Glu Glu Asn Val Pro Asp Gly His Val Ile Thr>

2120        2130        2140        2150        2160        2170        2180        2190        2200
CAG GAG TTA CGC GCC ACC GAC CCC GAC ACC ACG GCC GAT CTG CGC TTC GAG ATA AAC TGG GAC ACC TCT TTC GCC ACC AAG CAA GGC CGC
Gln Glu Leu Arg Ala Thr Asp Pro Asp Thr Thr Ala Asp Leu Arg Phe Glu Ile Asn Trp Asp Thr Ser Phe Ala Thr Lys Gln Gly Arg>

2210        2220        2230        2240        2250        2260        2270        2280        2290
CAG GCT AAC CCC GAC GAG TTT AGG AAT TGC GTG GAA ATC GAG ACC ATC TTC CCC GAG ATT AAC AAC CGG GGA CTG GCT ATC GGC CGC GTT
Gln Ala Asn Pro Asp Glu Phe Arg Asn Cys Val Glu Ile Glu Thr Ile Phe Pro Glu Ile Asn Asn Arg Gly Leu Ala Ile Gly Arg Val>

2300        2310        2320        2330        2340        2350        2360        2370        2380
GTA GCG CGC GAA ATC AGA CAC AAC GTG ACC ATA GAC TAC GAG GAG TTT GAG GTC CTC TCC CTC ACA GTG AGG GTG CGT GAC CTT AAC ACC
Val Ala Arg Glu Ile Arg His Asn Val Thr Ile Asp Tyr Glu Glu Phe Glu Val Leu Ser Leu Thr Val Arg Val Arg Asp Leu Asn Thr>

2390        2400        2410        2420        2430        2440        2450        2460        2470
GTC TAC GGA GAC GAC TAC GAC GAA TCG ATG CTC ACA ATA ACT ATA ATC GAT ATG AAC GAC AAC GCG CCG GTG TGG GTG GAG GGG ACT CTG
Val Tyr Gly Asp Asp Tyr Asp Glu Ser Met Leu Thr Ile Thr Ile Ile Asp Met Asn Asp Asn Ala Pro Val Trp Val Glu Gly Thr Leu>

2480        2490        2500        2510        2520        2530        2540        2550        2560
GAG CAG AAC TTC CGA GTC CGC GAG ATG TCG GCG GGC GGG CTC GTG GTG GGC TCC GTG CGC GCG GAC GAC ATC GAC GGA CCG CTC TAC AAC
Glu Gln Asn Phe Arg Val Arg Glu Met Ser Ala Gly Gly Leu Val Val Gly Ser Val Arg Ala Asp Asp Ile Asp Gly Pro Leu Tyr Asn>

2570        2580        2590        2600        2610        2620        2630        2640        2650
CAA GTG CGA TAC ACC ATT TTC CCT CGT GAA GAC ACA GAT AAG GAC CTG ATA ATG ATC GAC TTC CTC ACG GGT CAA ATT TCC GTG AAC ACA
Gln Val Arg Tyr Thr Ile Phe Pro Arg Glu Asp Thr Asp Lys Asp Leu Ile Met Ile Asp Phe Leu Thr Gly Gln Ile Ser Val Asn Thr>

2660        2670        2680        2690        2700        2710        2720        2730        2740
AGC GGC GCC ATC GAC GCG GAT ACT CCT CCA CGC TTC CAC CTC TAC TAT ACA GTG GTC GCT AGT GAC CGA TGC TCG ACA GAA GAT CCT GCA
Ser Gly Ala Ile Asp Ala Asp Thr Pro Pro Arg Phe His Leu Tyr Tyr Thr Val Val Ala Ser Asp Arg Cys Ser Thr Glu Asp Pro Ala>

2750        2760        2770        2780        2790        2800        2810        2820        2830
GAT TGC CCC CCT GAC CCG ACT TAT TGG GAA ACC GAA GGA AAT ATC ACA ATC CAC ATC ACC GAC ACG AAC AAC AAG GTC CCG CAG GCG GAA
Asp Cys Pro Pro Asp Pro Thr Tyr Trp Glu Thr Glu Gly Asn Ile Thr Ile His Ile Thr Asp Thr Asn Asn Lys Val Pro Gln Ala Glu>

2840        2850        2860        2870        2880        2890        2900        2910        2920
ACG ACT AAG TTC GAT ACC GTC GTG TAT ATT TAC GAG AAC GCA ACC CAC TTA GAC GAG GTG GTC ACT CTG ATA GCC AGT GAT CTT GAC AGA
Thr Thr Lys Phe Asp Thr Val Val Tyr Ile Tyr Glu Asn Ala Thr His Leu Asp Glu Val Val Thr Leu Ile Ala Ser Asp Leu Asp Arg>
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Fig. 1 cont.

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2930        2940        2950        2960        2970        2980        2990        3000        3010
   *           *           *           *           *           *           *           *           *
GAC GAA ATA TAC CAC ACG GTG AGC TAC GTC ATC AAT TAT GCA GTG AAC CCT CGA CTG ATG AAC TTC TTC TCC GTG AAC CGA GAG ACC GGC
Asp Glu Ile Tyr His Thr Val Ser Tyr Val Ile Asn Tyr Ala Val Asn Pro Arg Leu Met Asn Phe Phe Ser Val Asn Arg Glu Thr Gly>

3020        3030        3040        3050        3060        3070        3080        3090        3100
   *           *           *           *           *           *           *           *           *
CTG GTG TAC GTG GAC TAT GAG ACC CAG GGT AGT GGC GAG GTG CTG GAC CGT GAT GGT GAT GAA CCA ACG CAC CGT ATC TTC TTC AAC CTC
Leu Val Tyr Val Asp Tyr Glu Thr Gln Gly Ser Gly Glu Val Leu Asp Arg Asp Gly Asp Glu Pro Thr His Arg Ile Phe Phe Asn Leu>

3110        3120        3130        3140        3150        3160        3170        3180        3190
   *           *           *           *           *           *           *           *           *
ATC GAC AAC TTC ATG GGG GAA GGA GAA GGT AAC AGA AAT CAG AAC GAC ACA GAA GTT CTC GTT ATC TTG TTG GAT GTG AAT GAC AAT GCT
Ile Asp Asn Phe Met Gly Glu Gly Glu Gly Asn Arg Asn Gln Asn Asp Thr Glu Val Leu Val Ile Leu Leu Asp Val Asn Asp Asn Ala>

3200        3210        3220        3230        3240        3250        3260        3270        3280
   *           *           *           *           *           *           *           *           *
CCT GAA TTG CCA CCG CCG AGC GAA CTC TCT TGG ACT ATA TCT GAG AAC CTT AAG CAG GGC GTC CGT CTT GAA CCA CAT ATC TTC GCC CCG
Pro Glu Leu Pro Pro Pro Ser Glu Leu Ser Trp Thr Ile Ser Glu Asn Leu Lys Gln Gly Val Arg Leu Glu Pro His Ile Phe Ala Pro>

3290        3300        3310        3320        3330        3340        3350        3360        3370
   *           *           *           *           *           *           *           *           *
GAC CGC GAC GAG CCC GAC ACA GAC AAC TCC AGG GTC GGC TAC GAG ATC CTG AAC CTC AGC ACG GAG CGG GAC ATC GAA GTG CCG GAG CTG
Asp Arg Asp Glu Pro Asp Thr Asp Asn Ser Arg Val Gly Tyr Glu Ile Leu Asn Leu Ser Thr Glu Arg Asp Ile Glu Val Pro Glu Leu>

3380        3390        3400        3410        3420        3430        3440        3450        3460
   *           *           *           *           *           *           *           *           *
TTT GTG ATG ATA CAG ATC GCG AAC GTC ACG GGA GAG CTG GAG ACC GCC ATG GAC CTC AAG GGA TAT TGG GGG ACG TAC GCT ATA CAT ATA
Phe Val Met Ile Gln Ile Ala Asn Val Thr Gly Glu Leu Glu Thr Ala Met Asp Leu Lys Gly Tyr Trp Gly Thr Tyr Ala Ile His Ile>

3470        3480        3490        3500        3510        3520        3530        3540        3550
   *           *           *           *           *           *           *           *           *
CGG GCA TTC GAC CAC GGC ATT CCG CAA ATG TCC ATG AAC GAG ACA TAT GAG CTG ATC ATC CAT CCG TTC AAC TAC TAC GCG CCT GAG TTC
Arg Ala Phe Asp His Gly Ile Pro Gln Met Ser Met Asn Glu Thr Tyr Glu Leu Ile Ile His Pro Phe Asn Tyr Tyr Ala Pro Glu Phe>

3560        3570        3580        3590        3600        3610        3620        3630        3640
   *           *           *           *           *           *           *           *           *
GTC TTC CCG ACC AAC GAT GCC GTC ATA CGA CTT GCG AGG GAA CGA GCT GTA ATC AAT GGA GTT CTA GCG ACA GTG AAC GGA GAG TTC TTG
Val Phe Pro Thr Asn Asp Ala Val Ile Arg Leu Ala Arg Glu Arg Ala Val Ile Asn Gly Val Leu Ala Thr Val Asn Gly Glu Phe Leu>

3650        3660        3670        3680        3690        3700        3710        3720        3730
   *           *           *           *           *           *           *           *           *
GAG CGG ATA TCG GCG ACT GAT CCG GAC GGA CTC CAC GCG GGC GTC GTC ACC TTC CAA GTG GTA GGC GAT GAG GAA TCA CAA CGG TAC TTT
Glu Arg Ile Ser Ala Thr Asp Pro Asp Gly Leu His Ala Gly Val Val Thr Phe Gln Val Val Gly Asp Glu Glu Ser Gln Arg Tyr Phe>

3740        3750        3760        3770        3780        3790        3800        3810        3820
   *           *           *           *           *           *           *           *           *
CAA GTA GTT AAC GAT GGC GAG AAC CTC GGC TCG TTG AGG TTA CTG CAA GCC GTT CCA GAG GAG ATC AGG GAG TTC CGG ATA ACG ATT CGC
Gln Val Val Asn Asp Gly Glu Asn Leu Gly Ser Leu Arg Leu Leu Gln Ala Val Pro Glu Glu Ile Arg Glu Phe Arg Ile Thr Ile Arg>

3830        3840        3850        3860        3870        3880        3890        3900        3910
   *           *           *           *           *           *           *           *           *
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Fig. 1(cont)

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   GCT ACA GAC CAG GGA ACG GAC CCA GGA CCG CTG TCC ACG GAC ATG ACC TTC AGA GTT GTT TTT GTG CCC ACG CAA GGA GAA CCT AGA TTC
   Ala Thr Asp Gln Gly Thr Asp Pro Gly Pro Leu Ser Thr Asp Met Thr Phe Arg Val Val Phe Val Pro Thr Gln Gly Glu Pro Arg Phe>

3920        3930        3940        3950        3960        3970        3980        3990        4000
   *           *           *           *           *           *           *           *           *
   GCG TCC TCA GAA CAT GCT GTC GCT TTC ATA GAA AAG AGT GCC GGC ATG GAA GAG TCT CAC CAA CTT CCT CTA GCA CAA GAC ATC AAG AAC
   Ala Ser Ser Glu His Ala Val Ala Phe Ile Glu Lys Ser Ala Gly Met Glu Glu Ser His Gln Leu Pro Leu Ala Gln Asp Ile Lys Asn>

4010        4020        4030        4040        4050        4060        4070        4080        4090
   *           *           *           *           *           *           *           *           *
   CAT CTC TGT GAA GAC GAC TGT CAC AGC ATT TAC TAT CGT ATT ATC GAT GGC AAC AGC GAA GGT CAT TTC GGC CTG GAT CCT GTT CGC AAC
   His Leu Cys Glu Asp Asp Cys His Ser Ile Tyr Tyr Arg Ile Ile Asp Gly Asn Ser Glu Gly His Phe Gly Leu Asp Pro Val Arg Asn>

4100        4110        4120        4130        4140        4150        4160        4170        4180
   *           *           *           *           *           *           *           *           *
   AGG TTG TTC CTG AAG AAA GAG CTG ATA AGG GAA CAA AGT GCC TCC CAC ACT CTG CAA GTG GCG GCT AGT AAC TCG CCC GAT GGT GGC ATT
   Arg Leu Phe Leu Lys Lys Glu Leu Ile Arg Glu Gln Ser Ala Ser His Thr Leu Gln Val Ala Ala Ser Asn Ser Pro Asp Gly Gly Ile>

4190        4200        4210        4220        4230        4240        4250        4260        4270
   *           *           *           *           *           *           *           *           *
   CCA CTT CCT GCT TCC ATC CTT ACT GTC ACT GTT ACC GTG AGG GAG GCA GAC CCT CGT CCA GTG TTT GTG AGG GAA TTG TAC ACC GCA GGG
   Pro Leu Pro Ala Ser Ile Leu Thr Val Thr Val Thr Val Arg Glu Ala Asp Pro Arg Pro Val Phe Val Arg Glu Leu Tyr Thr Ala Gly>

4280        4290        4300        4310        4320        4330        4340        4350        4360
   *           *           *           *           *           *           *           *           *
   ATA TCC ACA GCG GAC TCC ATC GGC AGA GAG CTG CTC AGA TTA CAT GCG ACC CAG TCT GAA GGC TCG GCC ATT ACT TAT GCT ATA GAC TAC
   Ile Ser Thr Ala Asp Ser Ile Gly Arg Glu Leu Leu Arg Leu His Ala Thr Gln Ser Glu Gly Ser Ala Ile Thr Tyr Ala Ile Asp Tyr>

4370        4380        4390        4400        4410        4420        4430        4440        4450
   *           *           *           *           *           *           *           *           *
   GAT ACA ATG GTA GTG GAC CCC AGC CTG GAG GCA GTG AGA CAG TCG GCT TTC GTA CTG AAC GCT CAA ACC GGA GTG CTG ACG CTT AAT ATC
   Asp Thr Met Val Val Asp Pro Ser Leu Glu Ala Val Arg Gln Ser Ala Phe Val Leu Asn Ala Gln Thr Gly Val Leu Thr Leu Asn Ile>

4460        4470        4480        4490        4500        4510        4520        4530        4540
   *           *           *           *           *           *           *           *           *
   CAG CCC ACG GCC ACG ATG CAT GGA CTG TTC AAA TTC GAA GTC ACA GCT ACT GAC ACG GCC GGC GCT CAG GAC CGC ACC GAC GTC ACC GTG
   Gln Pro Thr Ala Thr Met His Gly Leu Phe Lys Phe Glu Val Thr Ala Thr Asp Thr Ala Gly Ala Gln Asp Arg Thr Asp Val Thr Val>

4550        4560        4570        4580        4590        4600        4610        4620        4630
   *           *           *           *           *           *           *           *           *
   TAC GTG GTA TCC TCG CAG AAC CGC GTC TAC TTC GTG TTC GTC AAC ACG CTG CAA CAG GTC GAA GAC AAC AGA GAC TTT ATC GCG GAC ACC
   Tyr Val Val Ser Ser Gln Asn Arg Val Tyr Phe Val Phe Val Asn Thr Leu Gln Gln Val Glu Asp Asn Arg Asp Phe Ile Ala Asp Thr>

4640        4650        4660        4670        4680        4690        4700        4710        4720
   *           *           *           *           *           *           *           *           *
   TTC AGC GCT GGG TTC AAC ATG ACC TGC AAC ATC GAC CAA GTG GTG CCC GCT AAC GAC CCC GTC ACC GGC GTG GCG CTG GAG CAC AGC ACG
   Phe Ser Ala Gly Phe Asn Met Thr Cys Asn Ile Asp Gln Val Val Pro Ala Asn Asp Pro Val Thr Gly Val Ala Leu Glu His Ser Thr>

4730        4740        4750        4760        4770        4780        4790        4800        4810        4820        4830
   *           *           *           *           *           *           *           *           *           *           *
   CAG ATG GCG GCC ACT TCA TAC GGG ACA ACG TAC CCG TAC TCG CTG ATG AGA TAG A ACAGATCCGTAGTGACCTAGTCCTCCTGAGCTCGATACAAACAACG
   Gln Met Ala Ala Thr Ser Tyr Gly Thr Thr Tyr Pro Tyr Ser Leu Met Arg *** Xxx>

        4840        4850        4860        4870        4880        4890        4900        4910        4920        4930        4940        4950
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Fig. 1(cont)

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CTGGCGGCGCGATCGTGGTGTTGCAGGACTTGTTGACCAACTCCAGCCCGGACTTCGGCGCCTGACTCGAGCCTGCACGGTGTACGTCTGGCCTCACTGTCTGCTGTGCTCGGTTTCATG

      4960      4970      4980      4990      5000      5010      5020      5030      5040      5050      5060      5070
TGCCTTGTGCTACTGCTTACCTTCATCATCAGGACTAC...CGCTAAACCGACGGTTGGAAGCCCTGTCGATGACGAAGTACGGCTCACTGGACTCTGGATTGAACCGCGCCGGCATCGCC

      5080      5090      5100      5110      5120      5130      5140      5150      5160      5170      5180      5190
GCCCCCGGCACCAACAAACACACTGTGGAAGGCTCCAACCCTATCTTCAATGAAGCAATAAAGACGCCAGATTTAGATGCCATTAGCGAGGGTTCCAACGACTCTGATCTGATCGGCATC

      5200      5210      5220      5230      5240      5250      5260      5270      5280      5290      5300      5310
GAAGATCTTGCGCACTTTGGCAACGTCTTCATGGATCCTGAGGTGAACGAAAAGGCAAATGGTTATCCCGAAGTCGCAAACCACAACAACAACTTCGCTTTCAACCCGACTCCCTTCTCG

      5320      5330      5340      5350      5360      5370      5380      5390      5400      5410      5420      5430
CCTGAGTTCGTTAACGGACAGTTCAGAAAGATCTAGAAGATAACAACACTAGTTAAGATCATTAATTTTGGAGTTTGGAATTAAGATTTTTGAAAGGATAGTTGTGATAAGCCTGTGATT

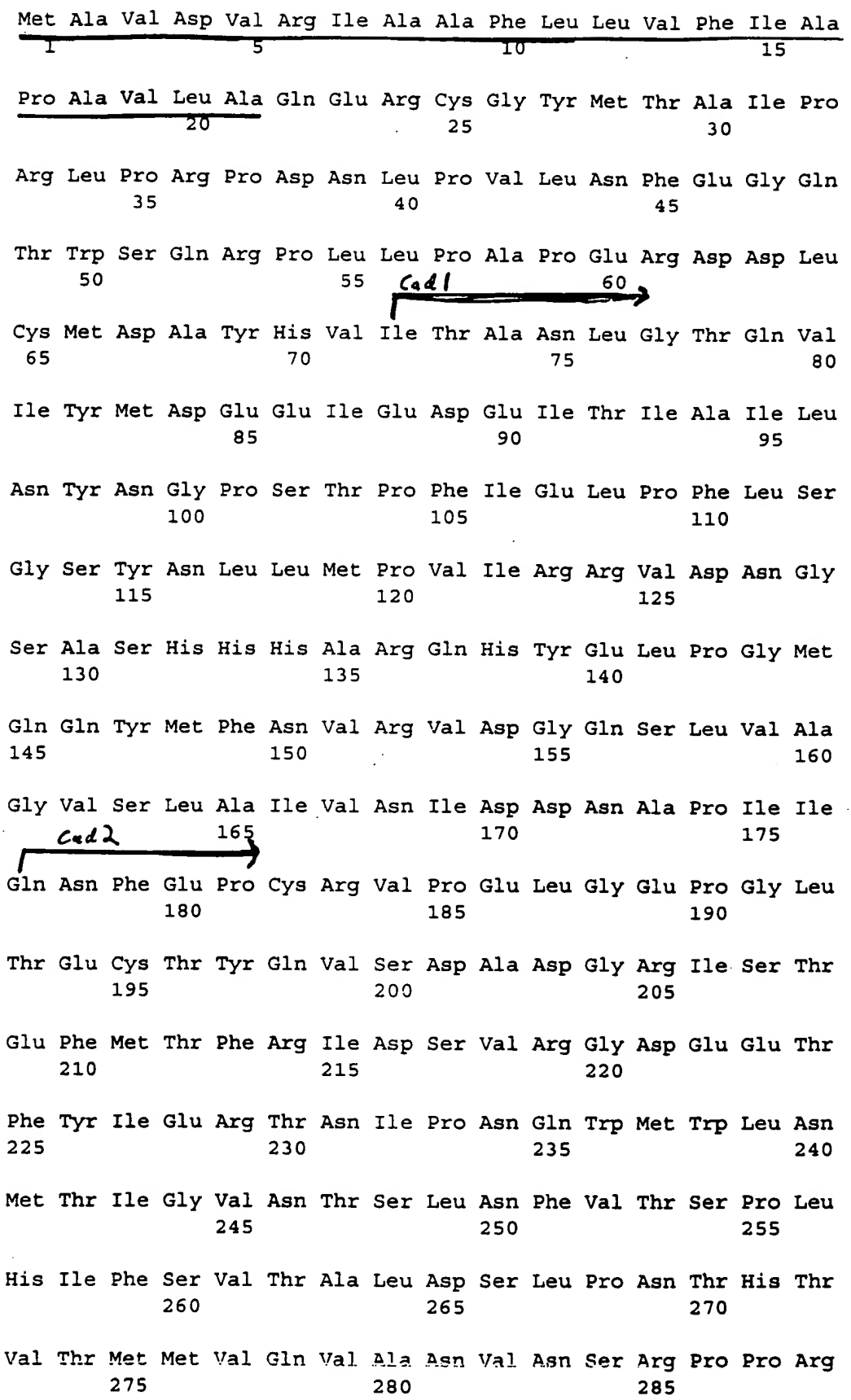
      5440      5450      5460      5470      5480      5490      5500      5510      5520      5530      5540      5550
TTTAAAACTGTAATTGAAAAAAAAAAATTGAGACCTCCATTTAAGCTCTTGCTCTCATCTCATCAAATTTTATAAAATGCCATTAGTCATTAAGATACTCGATTTAATTTAAGATTATTTA

      5560      5570
AGATATTATGTAAAATAAATATATTGTC
```

KEY TO UPDATED SEQUENCE:

updated nucleotide number:	type of change:
41	'G' addition
2105-08	rearrangement
2627-8	deletion
2668	'C' addition
2678	'G' addition
2946	rearrangement
3464	rearrangement
3471	rearrangement
4835-6	deletion
4884-4892	addition
4938	addition
5030	deletion
5031	rearrangement
5200	rearrangement
5216	rearrangement
5288	deletion
5422	rearrangement

Fig 1. (Cont'd)



dc-58851

FIGURE 2

Cad3

Trp Leu Glu Ile Phe Ala Val Gln Gln Phe Glu Glu Lys Ser Tyr Gln
290 295 300

Asn Phe Thr Val Arg Ala Ile Asp Gly Asp Thr Glu Ile Asn Met Pro
305 310 315 320

Ile Asn Tyr Arg Leu Ile Thr Asn Glu Glu Asp Thr Phe Phe Ser Ile
325 330 335

Glu Ala Leu Pro Gly Gly Lys Ser Gly Ala Val Phe Leu Val Ser Pro
340 345 350

Ile Asp Arg Asp Thr Leu Gln Arg Glu Val Phe Pro Leu Thr Ile Val
355 360 365

Ala Tyr Lys Tyr Asp Glu Glu Ala Phe Ser Thr Ser Thr Asn Val Val
370 375 380

Cad 4

Ile Ile Val Thr Asp Ile Asn Asp Gln Arg Pro Glu Pro Ile His Lys
385 390 395 400

Glu Tyr Arg Leu Ala Ile Met Glu Glu Thr Pro Leu Thr Leu Asn Phe
405 410 415

Asp Lys Glu Phe Gly Phe His Asp Lys Asp Leu Gly Gln Asn Ala Gln
420 425 430

Tyr Thr Val Arg Leu Glu Ser Val Asp Pro Pro Gly Ala Ala Glu Ala
435 440 445

Phe Tyr Ile Ala Pro Glu Val Gly Tyr Gln Arg Gln Thr Phe Ile Met
450 455 460

Gly Thr Leu Asn His Ser Met Leu Asp Tyr Glu Val Pro Glu Phe Gln
465 470 475 480

Ser Ile Thr Ile Arg Val Val Ala Thr Asp Asn Asn Asp Thr Arg His
485 490 495

Cad 5

Val Gly Val Ala Leu Val His Ile Asp Leu Ile Asn Trp Asn Asp Glu
500 505 510

Gln Pro Ile Phe Glu His Ala Val Gln Thr Val Thr Phe Asp Glu Thr
515 520 525

Glu Gly Glu Gly Phe Phe Val Ala Lys Ala Val Ala His Asp Arg Asp
530 535 540

Ile Gly Asp Val Val Glu His Thr Leu Leu Gly Asn Ala Val Asn Phe
545 550 555 560

Leu Thr Ile Asp Lys Leu Thr Gly Asp Ile Arg Val Ser Ala Asn Asp
565 570 575

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FIGURE 2

```
Ser Phe Asn Tyr His Arg Glu Ser Glu Leu Phe Val Gln Val Arg Ala
            580                 585                 590

Thr Asp Thr Leu Gly Glu Pro Phe His Thr Ala Thr Ser Gln Leu Val
        595                 600                 605

Ile Arg Leu Asn Asp Ile Asn Asn Thr Pro Pro Thr Leu Arg Leu Pro
    610                 615                 620

Arg Gly Ser Pro Gln Val Glu Glu Asn Val Pro Asp Gly His Val Ile
625                 630                 635                 640

Thr Gln Glu Leu Arg Ala Thr Asp Pro Asp Thr Thr Ala Asp Leu Arg
                645                 650                 655

Phe Glu Ile Asn Trp Asp Thr Ser Phe Ala Thr Lys Gln Gly Arg Gln
            660                 665                 670

Ala Asn Pro Asp Glu Phe Arg Asn Cys Val Glu Ile Glu Thr Ile Phe
        675                 680                 685

Pro Glu Ile Asn Asn Arg Gly Leu Ala Ile Gly Arg Val Val Ala Arg
    690                 695                 700

Glu Ile Arg His Asn Val Thr Ile Asp Tyr Glu Glu Phe Glu Val Leu
705                 710                 715                 720

Ser Leu Thr Val Arg Val Arg Asp Leu Asn Thr Val Tyr Gly Asp Asp
                725                 730                 735

Tyr Asp Glu Ser Met Leu Thr Ile Thr Ile Ile Asp Met Asn Asp Asn
            740                 745                 750

Ala Pro Val Trp Val Glu Gly Thr Leu Glu Gln Asn Phe Arg Val Arg
        755                 760                 765

Glu Met Ser Ala Gly Gly Leu Val Val Gly Ser Val Arg Ala Asp Asp
    770                 775                 780

Ile Asp Gly Pro Leu Tyr Asn Gln Val Arg Tyr Thr Ile Phe Pro Arg
785                 790                 795                 800

Glu Asp Thr Asp Lys Asp Leu Ile Met Ile Asp Phe Leu Thr Gly Gln
                805                 810                 815

Ile Ser Val Asn Thr Ser Gly Ala Ile Asp Ala Asp Thr Pro Pro Arg
            820                 825                 830

Phe His Leu Tyr Tyr Thr Val Val Ala Ser Asp Arg Cys Ser Thr Glu
        835                 840                 845

Asp Pro Ala Asp Cys Pro Pro Asp Pro Thr Tyr Trp Glu Thr Glu Gly
    850                 855                 860
```

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FIGURE 2

```
Asn Ile Thr Ile His Ile Thr Asp Thr Asn Asn Lys Val Pro Gln Ala
865 Cad 8                870                 875                 880

Glu Thr Thr Lys Phe Asp Thr Val Val Tyr Ile Tyr Glu Asn Ala Thr
                885                 890                 895

His Leu Asp Glu Val Val Thr Leu Ile Ala Ser Asp Leu Asp Arg Asp
            900                 905                 910

Glu Ile Tyr His Thr Val Ser Tyr Val Ile Asn Tyr Ala Val Asn Pro
        915                 920                 925

Arg Leu Met Asn Phe Phe Ser Val Asn Arg Glu Thr Gly Leu Val Tyr
    930                 935                 940

Val Asp Tyr Glu Thr Gln Gly Ser Gly Glu Val Leu Asp Arg Asp Gly
945                 950                 955                 960

Asp Glu Pro Thr His Arg Ile Phe Phe Asn Leu Ile Asp Asn Phe Met
                965                 970                 975

Gly Glu Gly Glu Gly Asn Arg Asn Gln Asn Asp Thr Glu Val Leu Val
            980                 985                 990
                                                Cad 9

Ile Leu Leu Asp Val Asn Asp Asn Ala Pro Glu Leu Pro Pro Pro Ser
        995                1000                1005

Glu Leu Ser Trp Thr Ile Ser Glu Asn Leu Lys Gln Gly Val Arg Leu
    1010                1015                1020

Glu Pro His Ile Phe Ala Pro Asp Arg Asp Glu Pro Asp Thr Asp Asn
1025                1030                1035                1040

Ser Arg Val Gly Tyr Glu Ile Leu Asn Leu Ser Thr Glu Arg Asp Ile
                1045                1050                1055

Glu Val Pro Glu Leu Phe Val Met Ile Gln Ile Ala Asn Val Thr Gly
            1060                1065                1070

Glu Leu Glu Thr Ala Met Asp Leu Lys Gly Tyr Trp Gly Thr Tyr Ala
        1075                1080                1085

Ile His Ile Arg Ala Phe Asp His Gly Ile Pro Gln Met Ser Met Asn
    1090                1095                1100

Glu Thr Tyr Glu Leu Ile Ile His Pro Phe Asn Tyr Tyr Ala Pro Glu
1105 Cad 10             1110                1115                1120

Phe Val Phe Pro Thr Asn Asp Ala Val Ile Arg Leu Ala Arg Glu Arg
                1125                1130                1135

Ala Val Ile Asn Gly Val Leu Ala Thr Val Asn Gly Glu Phe Leu Glu
            1140                1145                1150
```

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FIGURE 2

```
Arg Ile Ser Ala Thr Asp Pro Asp Gly Leu His Ala Gly Val Val Thr
        1155                1160                1165

Phe Gln Val Val Gly Asp Glu Glu Ser Gln Arg Tyr Phe Gln Val Val
    1170                1175                1180

Asn Asp Gly Glu Asn Leu Gly Ser Leu Arg Leu Leu Gln Ala Val Pro
1185                1190                1195                1200

Glu Glu Ile Arg Glu Phe Arg Ile Thr Ile Arg Ala Thr Asp Gln Gly
                1205                1210                1215

Thr Asp Pro Gly Pro Leu Ser Thr Asp Met Thr Phe Arg Val Val Phe
        1220                1225                1230

Val Pro Thr Gln Gly Glu Pro Arg Phe Ala Ser Ser Glu His Ala Val
        1235                1240                1245

Ala Phe Ile Glu Lys Ser Ala Gly Met Glu Glu Ser His Gln Leu Pro
    1250                1255                1260

Leu Ala Gln Asp Ile Lys Asn His Leu Cys Glu Asp Asp Cys His Ser
1265                1270                1275                1280

Ile Tyr Tyr Arg Ile Ile Asp Gly Asn Ser Glu Gly His Phe Gly Leu
                1285                1290                1295

Asp Pro Val Arg Asn Arg Leu Phe Leu Lys Lys Glu Leu Ile Arg Glu
            1300                1305                1310

Gln Ser Ala Ser His Thr Leu Gln Val Ala Ala Ser Asn Ser Pro Asp
        1315                1320                1325

Gly Gly Ile Pro Leu Pro Ala Ser Ile Leu Thr Val Thr Val Thr Val
    1330                1335                1340

Arg Glu Ala Asp Pro Arg Pro Val Phe Val Arg Glu Leu Tyr Thr Ala
1345                1350                1355                1360

Gly Ile Ser Thr Ala Asp Ser Ile Gly Arg Glu Leu Leu Arg Leu His
                1365                1370                1375

Ala Thr Gln Ser Glu Gly Ser Ala Ile Thr Tyr Ala Ile Asp Tyr Asp
            1380                1385                1390

Thr Met Val Val Asp Pro Ser Leu Glu Ala Val Arg Gln Ser Ala Phe
        1395                1400                1405

Val Leu Asn Ala Gln Thr Gly Val Leu Thr Leu Asn Ile Gln Pro Thr
    1410                1415                1420

Ala Thr Met His Gly Leu Phe Lys Phe Glu Val Thr Ala Thr Asp Thr
1425                1430                1435                1440
```

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FIGURE 2

Ala Gly Ala Gln Asp Arg Thr Asp Val Thr Val Tyr Val Val Ser Ser
1445 1450 1455

Gln Asn Arg Val Tyr Phe Val Phe Val Asn Thr Leu Gln Gln Val Glu
1460 1465 1470

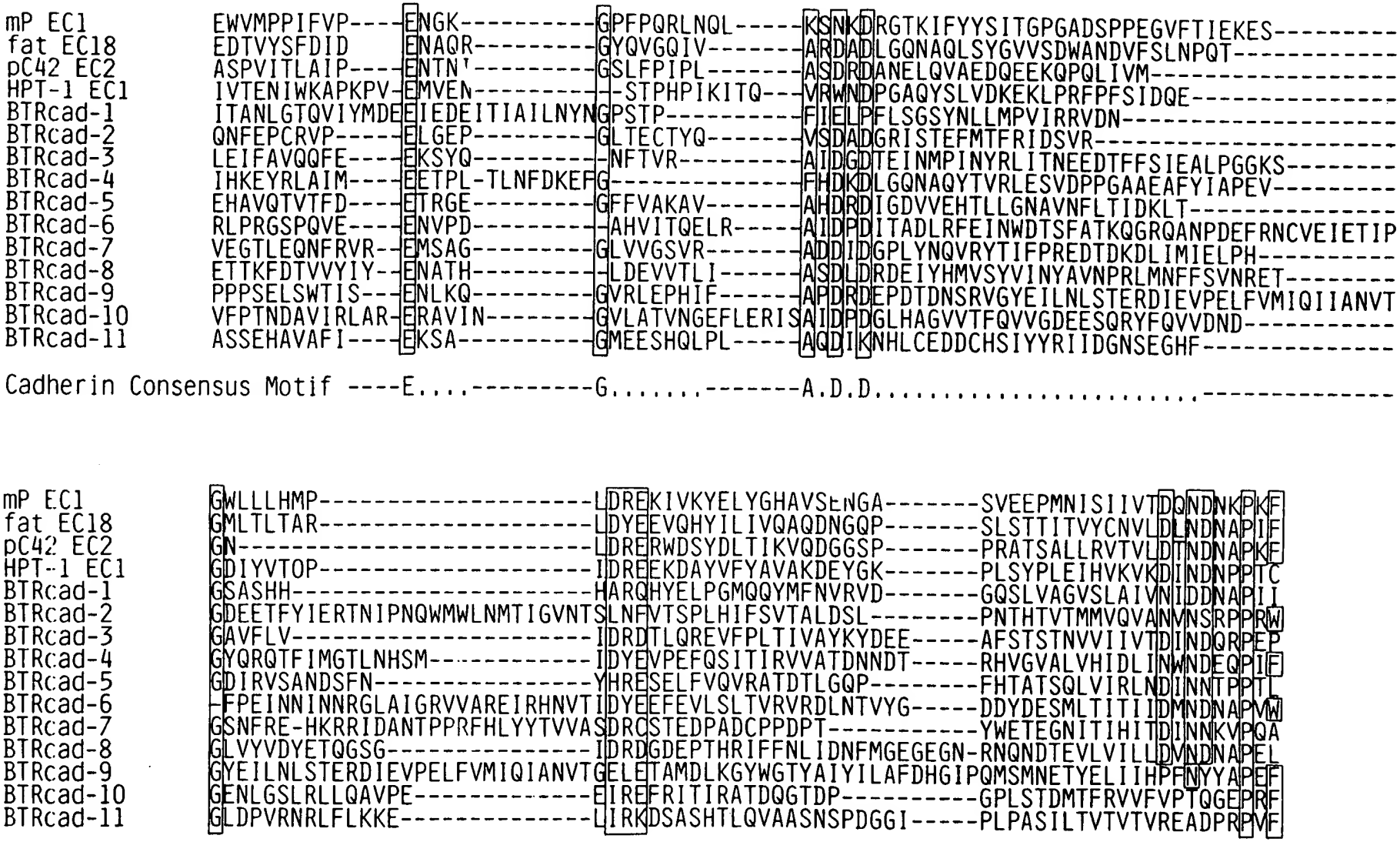
Asp Asn Arg Asp Phe Ile Ala Asp Thr Phe Ser Ala Gly Phe Asn Met
1475 1480 1485

Thr Cys Asn Ile Asp Gln Val Val Pro Ala Asn Asp Pro Val Thr Gly
1490 1495 1500

Val Ala Leu Glu His Ser Thr Gln Met Ala Ala Thr Ser Tyr Gly Thr
1505 1510 1515 1520

Thr Tyr Pro Tyr Ser Leu Met Arg
1525

FIGURE 2


mP EC1
fat EC18
pC42 EC2
HPT-1 EC1
BTRcad-1
BTRcad-2
BTRcad-3
BTRcad-4
BTRcad-5
BTRcad-6
BTRcad-7
BTRcad-8
BTRcad-9
BTRcad-10
BTRcad-11
Cadherin Consensus Motif
mP EC1
fat EC18
pC42 EC2
HPT-1 EC1
BTRcad-1
BTRcad-2
BTRcad-3
BTRcad-4
BTRcad-5
BTRcad-6
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BTRcad-8
BTRcad-9
BTRcad-10
BTRcad-11
Cadherin Consensus Motif

Fig 2(C)

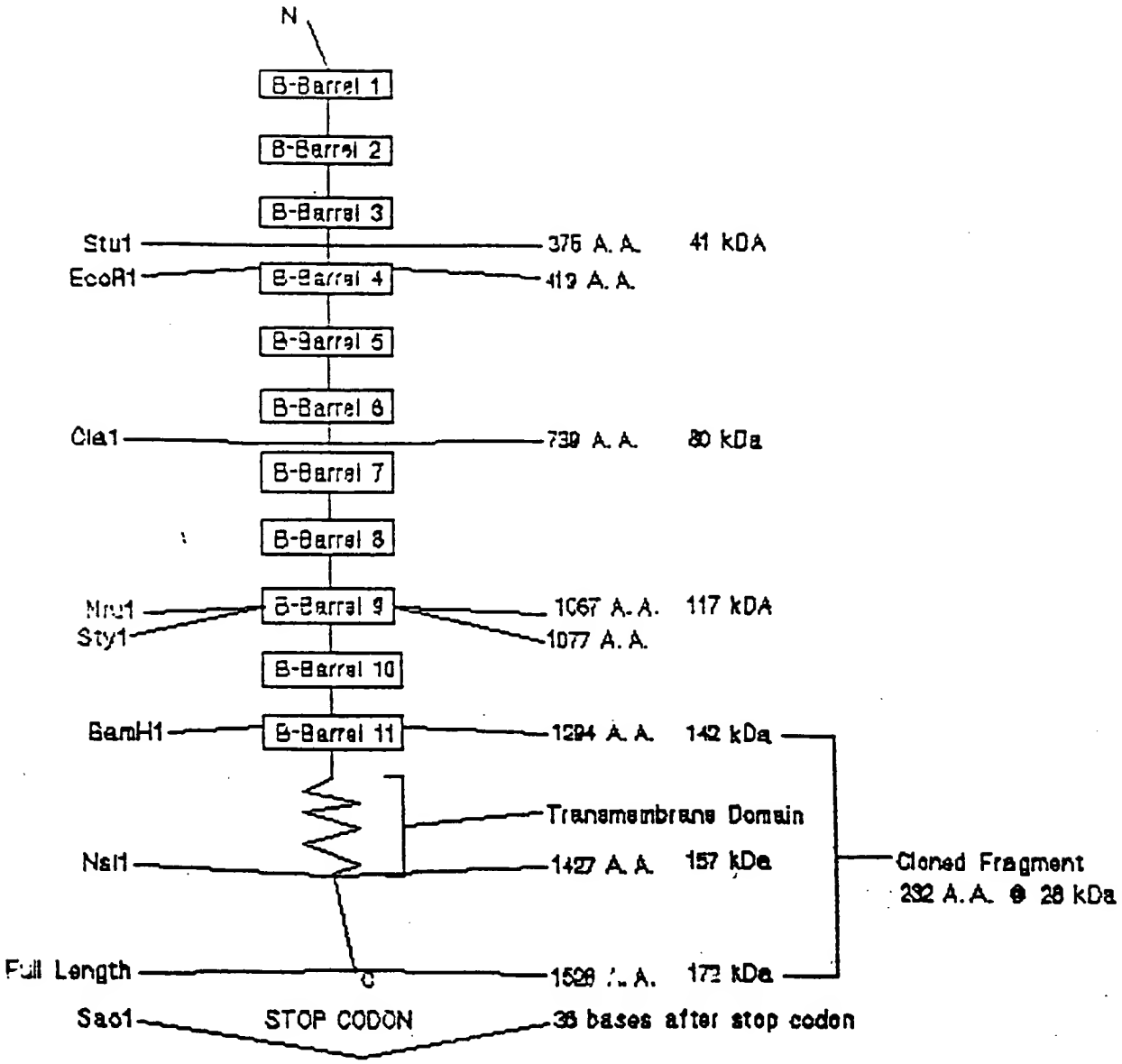
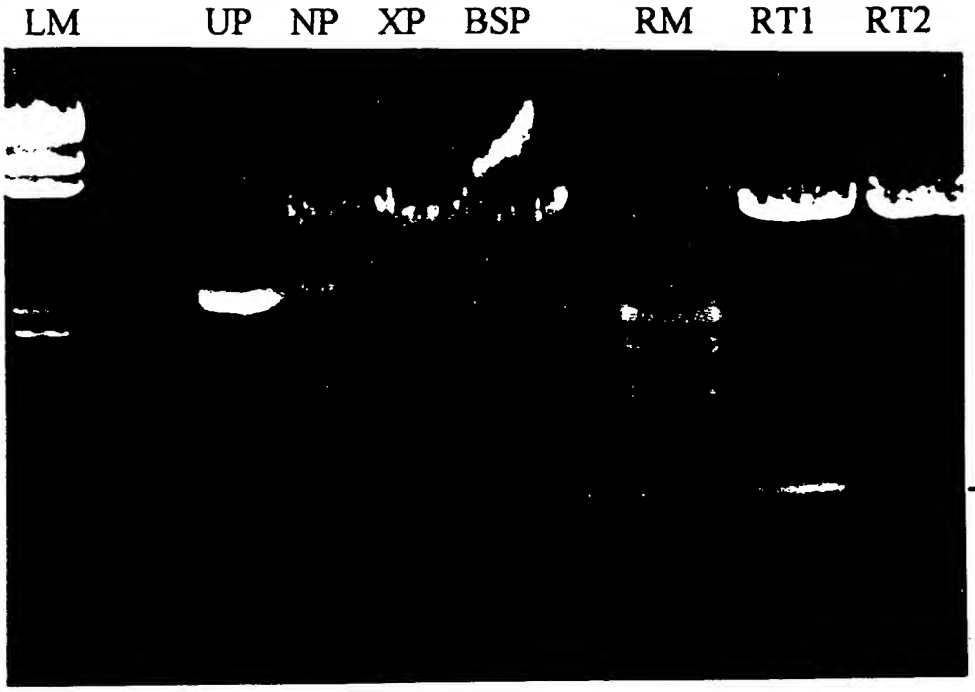


Fig. 3 Block diagram of cadherin-like structure of BT-R_1



-cDNA fragment and mRNA expression

Fig. 4 Clone characterization of BamHI-SacI fragment of BT-R_1. LM is HindIII cut Lambda marker; UP is the uncut plasmid clone; NP is NsiI cut plasmid; XP is XhoI cut plasmid; BSP is BamHI and SacI cut plasmid showing the cloned fragment from BT-R_1; RM is mRNA size marker; and RT1 and RT2 are transcribed mRNAs from the cloned BT-R_1 fragment.

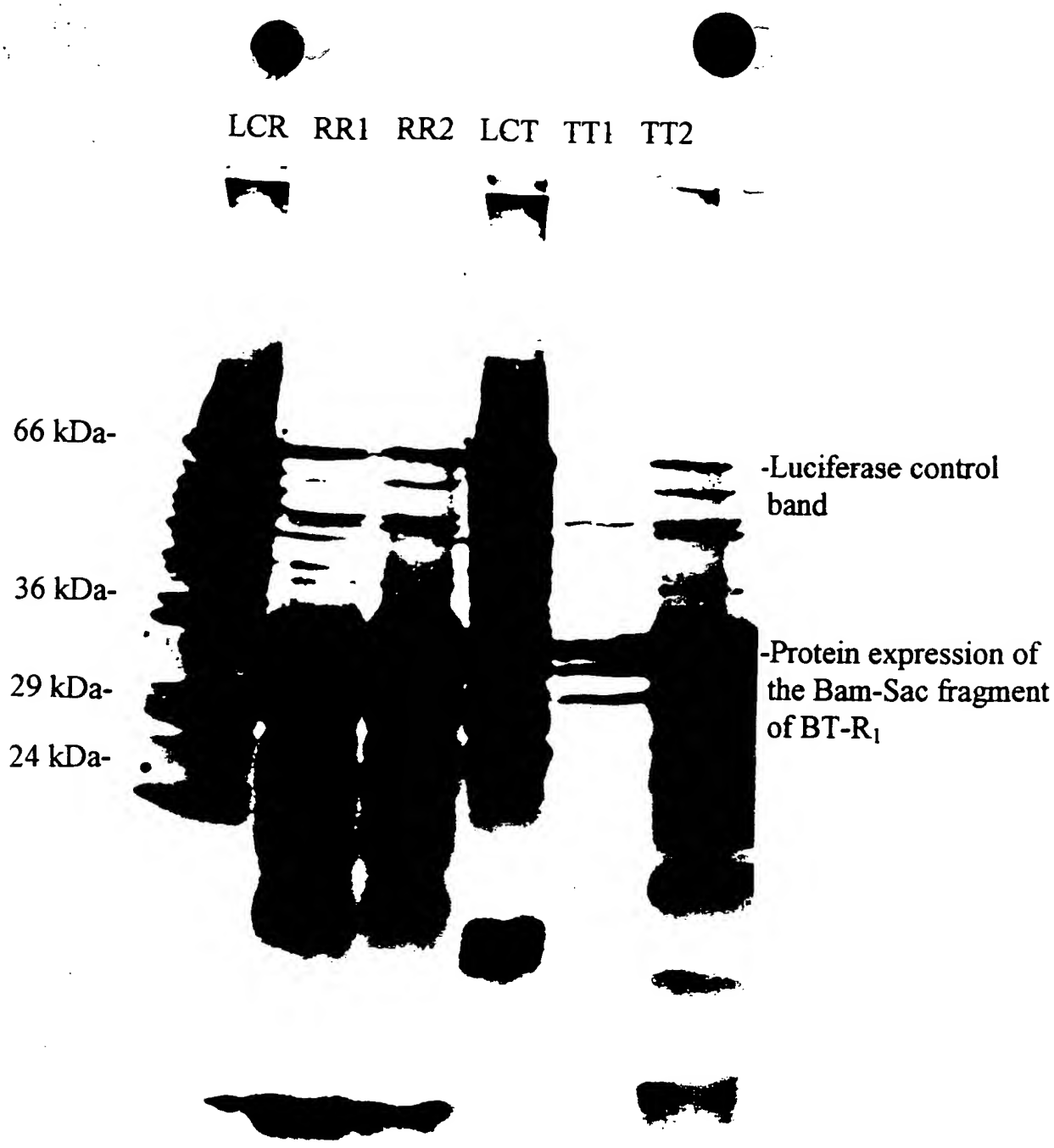


Fig. 5 Detection of protein expression from the plasmid containing the Bam-Sac fragment of BT-R_1 using ^{35}S-methionine as a tag. LCR is a luciferase control mRNA to show that the rabbit reticulocyte lysates are functional; RR1 and RR2 are expression products of the Bam-Sac fragment of BT-R_1 prodced in rabbit reticulocytes from mRNA; LCT is a luciferase control plasmid to show that the transcription/translation kit is functional; and TT1 and TT2 are expression products of the Bam-Sac fragment of BT-R_1 produced in a transcription/translation kit.

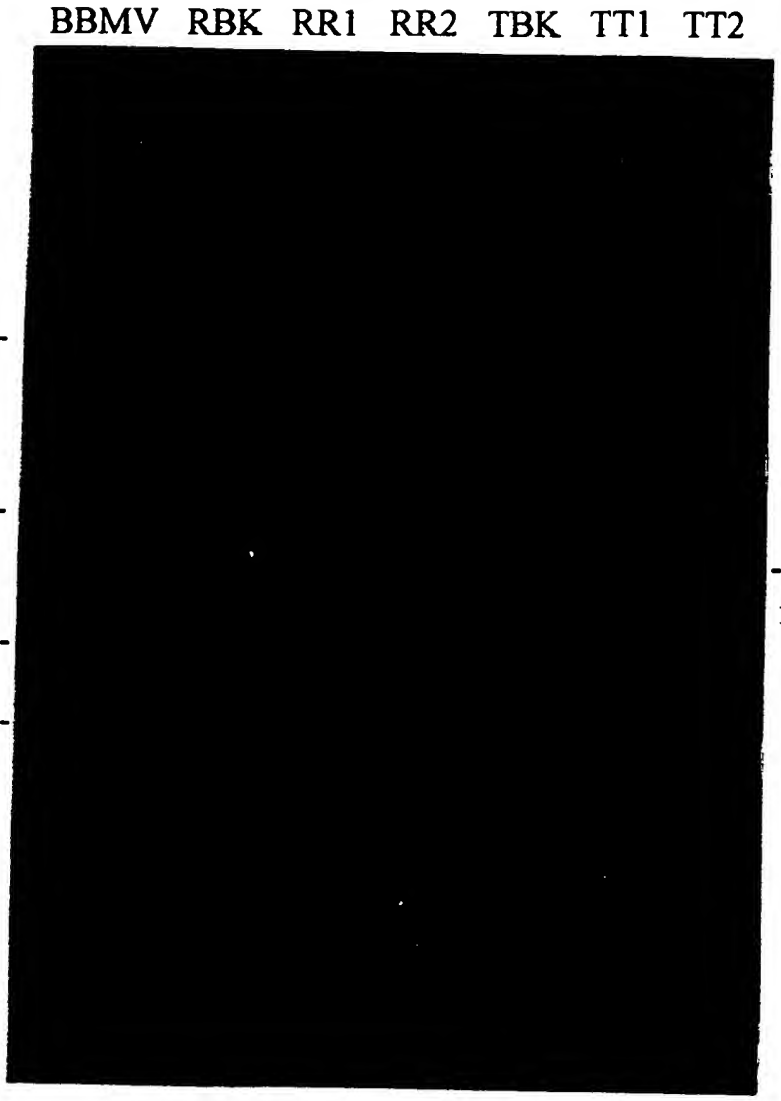
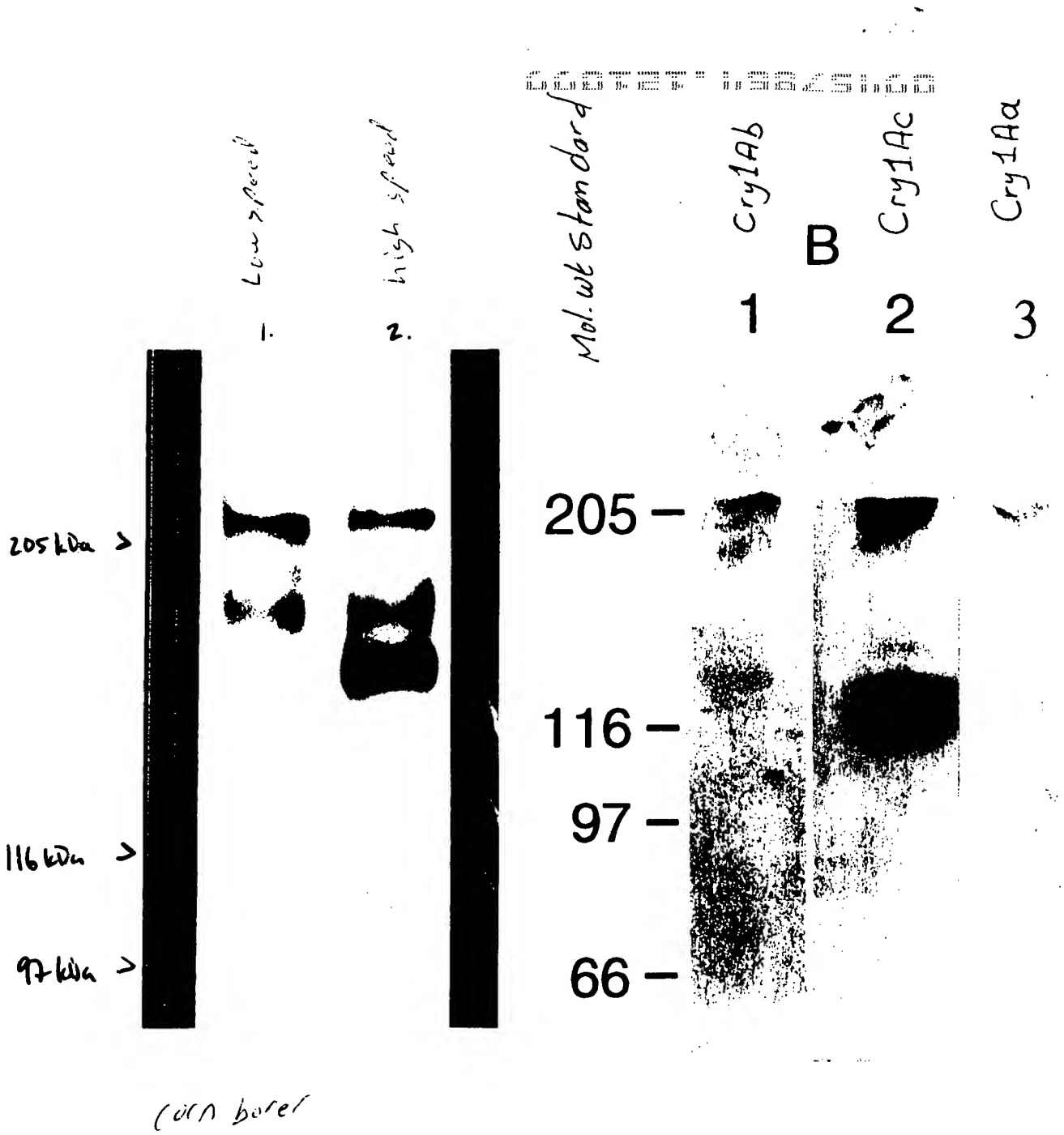


Fig. 6 Radio-blot of the Bam-Sac fragment of BT-R_1 with ^{125}I-labeled Cry1Ab. BBMV is the brush border membrane vesicles from the midgut of *M. Sexta* containing the wild-type BT-R_1 receptor protein;RBK is a rabbit reticulocyte blank; RR1 and RR2 are the expression products of the Bam-Sac fragment of BT-R_1 prodced in rabbit reticulocytes from mRNA; TBK is a transcription/translation kit blank; TT1 and TT2 are expression products of the Bam-Sac fragment of BT-R_1 produced in a transcription/translation kit. The arrows point to two of the bands.



BBMV proteins (200µg) from the Pink bollworm (Pectinophora gossypiella) were separated on 7.5% SDS-PAGE, blotted and probed with 2×10^5 cpm per ml of ^{125}I-labeled Cry Toxins.

Fig 7

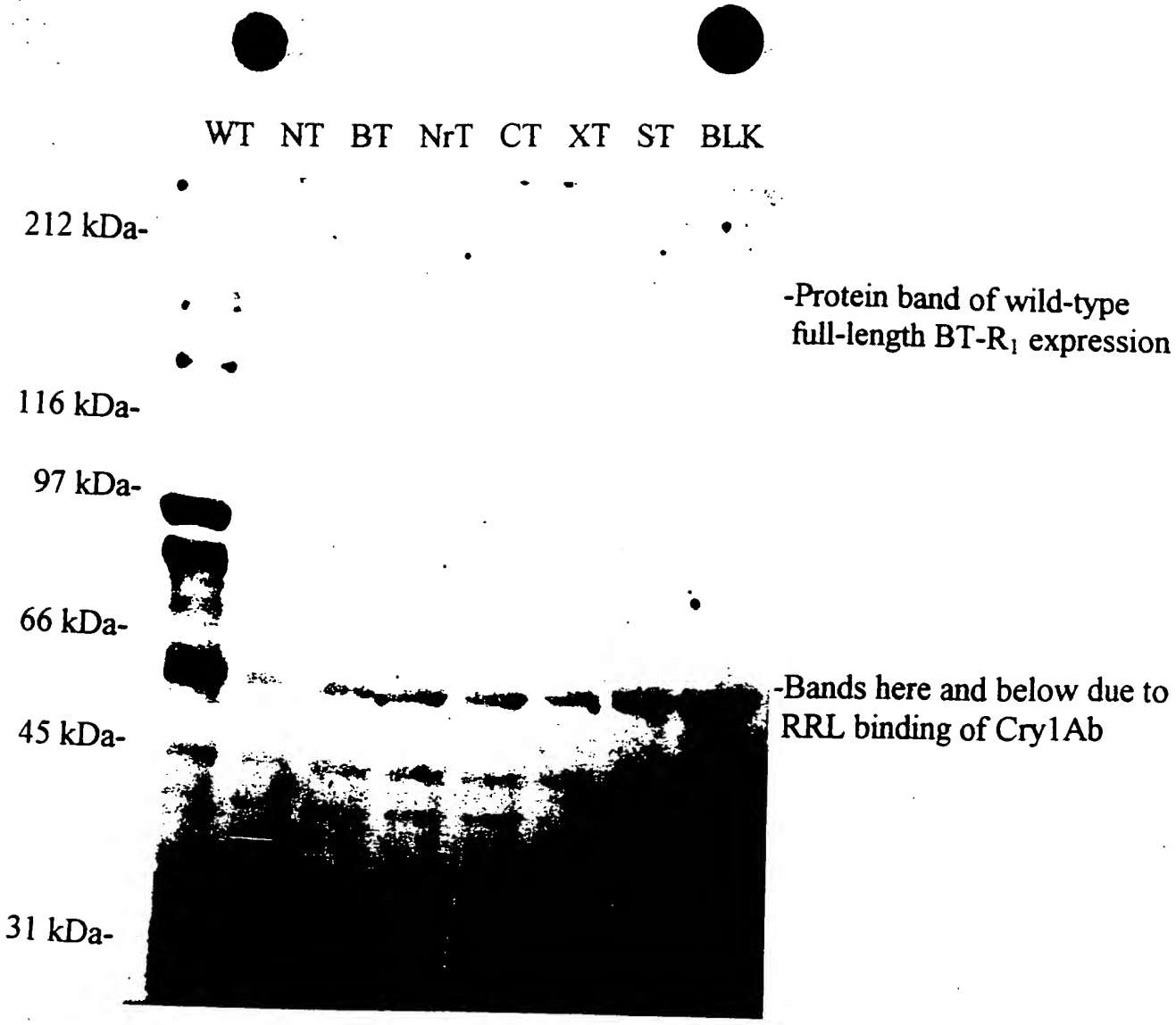


Fig. 8 Radio-blot of BT-R_1 and truncation mutants of BT-R_1 with ^{125}I-labeled Cry1Ab. WT is the wild-type full-length BT-R_1 receptor; NT is the truncation mutant resulting from NsiI digestion; BT is the mutant made with BamHI; NrT is the mutant made with NruI; CT is the mutant made with ClaI; XT is the mutant made with XhoI; ST is the mutant made with StuI; and, BLK is rabbit reticulocyte lysates containing only endogenous proteins.